

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: ELL2, A New Member of an ELL Family of RNA Polymerase II Elongation Factors

(iii) NUMBER OF SEQUENCES: 34

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(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/038,447  
(B) FILING DATE: 19-FEB-1997

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(C) REFERENCE/DOCKET NUMBER: 1488.0880001

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 94..2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTGGCGGC	GGGTGCAGAA	GCCCAAGCAG	CGCGGCCGCA	GTGGAGGCTA	GAGCCGGAGC	60
GGCGGCGGCG	GCAGCACCCC	GGGGAGGTTT	AAG ATG GCG GCG GGG GGG ACA GGG	Met Ala Ala Gly Gly Thr Gly	114	
			1	5		
GGC CTG CGG GAG GAG CAG CGC TAT GGG CTG TCG TGC GGA CGG CTG GGG	162					
Gly Leu Arg Glu Glu Gln Arg Tyr Gly Leu Ser Cys Gly Arg Leu Gly						
10 15 20						
CAG GAC AAC ATC ACC GTA CTG CAT GTG AAG CTC ACC GAG ACG GCG ATC	210					
Gln Asp Asn Ile Thr Val Leu His Val Lys Leu Thr Glu Thr Ala Ile						
25 30 35						
CGG GCG CTC GAG ACT TAC CAG AGC CAC AAG AAT TTA ATT CCT TTT CGA	258					
Arg Ala Leu Glu Thr Tyr Gln Ser His Lys Asn Leu Ile Pro Phe Arg						
40 45 50 55						
CCT TCA ATC CAG TTC CAA GGA CTC CAC GGG CTT GTC AAA ATT CCC AAA	306					
Pro Ser Ile Gln Phe Gln Gly Leu His Gly Leu Val Lys Ile Pro Lys						
60 65 70						
AAT GAT CCC CTC AAT GAA GTT CAT AAC TTT AAC TTT TAT TTG TCA AAT	354					
Asn Asp Pro Leu Asn Glu Val His Asn Phe Asn Phe Tyr Leu Ser Asn						
75 80 85						
GTG GGC AAA GAC AAC CCT CAG GGC AGC TTT GAC TGC ATC CAG CAA ACA	402					
Val Gly Lys Asp Asn Pro Gln Gly Ser Phe Asp Cys Ile Gln Gln Thr						
90 95 100						
TTC TCC AGC TCT GGA GCC TCC CAG CTC AAT TGC CTG GGA TTT ATA CAA	450					
Phe Ser Ser Ser Gly Ala Ser Gln Leu Asn Cys Leu Gly Phe Ile Gln						
105 110 115						
GAT AAA ATT ACA GTG TGT GCA ACA AAC GAC TCG TAT CAG ATG ACA CGA	498					
Asp Lys Ile Thr Val Cys Ala Thr Asn Asp Ser Tyr Gln Met Thr Arg						
120 125 130 135						
GAA AGA ATG ACC CAG GCA GAG GAG GAA TCC CGC AAC CGA AGC ACA AAA	546					
Glu Arg Met Thr Gln Ala Glu Glu Ser Arg Asn Arg Ser Thr Lys						
140 145 150						
GTT ATC AAA CCC GGT GGA CCA TAT GTA GGG AAA AGA GTG CAA ATT CGG	594					
Val Ile Lys Pro Gly Gly Pro Tyr Val Gly Lys Arg Val Gln Ile Arg						
155 160 165						
AAA GCA CCT CAA GCT GTT TCA GAT ACA GTT CCT GAG AGG AAA AGG TCA	642					
Lys Ala Pro Gln Ala Val Ser Asp Thr Val Pro Glu Arg Lys Arg Ser						
170 175 180						
ACC CCC ATG AAC CCT GCA AAT ACA ATT CGA AAG ACA CAT AGC AGC AGC	690					
Thr Pro Met Asn Pro Ala Asn Thr Ile Arg Lys Thr His Ser Ser Ser						
185 190 195						
ACC ATC TCT CAG AGG CCA TAC AGG GAC AGG GTG ATT CAC TTA CTG GCC	738					
Thr Ile Ser Gln Arg Pro Tyr Arg Asp Arg Val Ile His Leu Leu Ala						
200 205 210 215						
CTG AAG GCC TAC AAG AAA CCG GAG CTA CTT GCT AGA CTC CAG AAA GAT	786					

Leu	Lys	Ala	Tyr	Lys	Lys	Pro	Glu	Leu	Leu	Ala	Arg	Leu	Gln	Lys	Asp	
		220				225						230				
GGT	GTC	AAT	CAA	AAA	GAC	AAG	AAC	TCC	CTG	GGA	GCA	ATT	CTG	CAA	CAG	834
Gly	Val	Asn	Gln	Lys	Asp	Lys	Asn	Ser	Leu	Gly	Ala	Ile	Leu	Gln	Gln	
		235				240						245				
GTA	GCC	AAT	CTG	AAT	TCT	AAG	GAC	CTC	TCA	TAT	ACC	TTA	AAG	GAT	TAT	882
Val	Ala	Asn	Leu	Asn	Ser	Lys	Asp	Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	
		250				255					260					
GTT	TTT	AAA	GAG	CTT	CAA	AGA	GAC	TGG	CCT	GGA	TAC	AGT	GAA	ATA	GAC	930
Val	Phe	Lys	Glu	Leu	Gln	Arg	Asp	Trp	Pro	Gly	Tyr	Ser	Glu	Ile	Asp	
		265				270					275					
AGA	CGG	TCA	TTG	GAG	TCA	GTG	CTC	TCT	AGA	AAA	CTA	AAT	CCG	TCT	CAG	978
Arg	Arg	Ser	Leu	Glu	Ser	Val	Leu	Ser	Arg	Lys	Leu	Asn	Pro	Ser	Gln	
		280				285				290			295			
AAT	GCT	ACA	GGC	ACC	AGC	CGT	TCA	GAA	TCT	CCT	GTA	TGT	TCT	AGT	AGA	1026
Asn	Ala	Thr	Gly	Thr	Ser	Arg	Ser	Glu	Ser	Pro	Val	Cys	Ser	Ser	Arg	
		300				305						310				
GAT	GCT	GTA	TCT	TCT	CCT	CAG	AAA	CGG	CTT	TTG	GAT	TCA	GAG	TTT	ATT	1074
Asp	Ala	Val	Ser	Ser	Pro	Gln	Lys	Arg	Leu	Leu	Asp	Ser	Glu	Phe	Ile	
		315				320					325					
GAT	CCT	TTA	ATG	AAT	AAA	AAA	GCC	CGA	ATA	TCT	CAC	CTG	ACG	AAC	AGA	1122
Asp	Pro	Leu	Met	Asn	Lys	Lys	Ala	Arg	Ile	Ser	His	Leu	Thr	Asn	Arg	
		330				335					340					
GTA	CCA	CCA	ACA	CTA	AAT	GGT	CAT	TTG	AAT	CCC	ACC	AGT	GAA	AAA	TCG	1170
Val	Pro	Pro	Thr	Leu	Asn	Gly	His	Leu	Asn	Pro	Thr	Ser	Glu	Lys	Ser	
		345				350				355						
GCT	GCA	GGC	CTC	CCA	CTG	CCC	CCT	GCG	GCT	GCT	GCC	ATC	CCC	ACC	CCT	1218
Ala	Ala	Gly	Leu	Pro	Leu	Pro	Pro	Ala	Ala	Ala	Ala	Ile	Pro	Thr	Pro	
		360			365				370			375				
CCA	CCG	CTG	CCT	TCA	ACC	TAT	CTG	CCC	ATC	TCA	CAT	CCT	CCT	CAG	ATT	1266
Pro	Pro	Leu	Pro	Ser	Thr	Tyr	Leu	Pro	Ile	Ser	His	Pro	Pro	Gln	Ile	
		380				385					390					
GTA	AAT	TCT	AAC	TCC	AAC	TCC	CCT	AGC	ACT	CCA	GAA	GGC	CGG	GGG	ACT	1314
Val	Asn	Ser	Asn	Ser	Asn	Pro	Ser	Thr	Pro	Glu	Gly	Arg	Gly	Thr		
		395				400					405					
CAA	GAC	CTA	CCT	GTT	GAC	AGT	TTT	AGT	CAA	AAC	GAT	AGT	ATC	TAT	GAG	1362
Gln	Asp	Leu	Pro	Val	Asp	Ser	Phe	Ser	Gln	Asn	Asp	Ser	Ile	Tyr	Glu	
		410			415							420				
GAC	CAG	CAA	GAC	AAA	TAT	ACC	TCT	AGG	ACT	TCT	CTG	GAA	ACC	TTA	CCC	1410
Asp	Gln	Gln	Asp	Lys	Tyr	Thr	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Leu	Pro	
		425			430					435						
CCT	GGT	TCC	GTT	CTA	CTA	AAG	TGT	CCA	AAG	CCT	ATG	GAA	GAA	AAC	CAT	1458
Pro	Gly	Ser	Val	Leu	Leu	Lys	Cys	Pro	Lys	Pro	Met	Glu	Glu	Asn	His	
		440			445				450			455				
TCA	ATG	TCT	CAC	AAA	ÀAG	TCC	AAA	AAG	AAG	TCT	AAA	AAA	CAT	AAG	GAA	1506
Ser	Met	Ser	His	Lys	Lys	Ser	Lys	Lys	Lys	Ser	Lys	Lys	His	Lys	Glu	
		460			465					470						

AAG GAC CAA ATA AAA AAG CAC GAC ATT GAG ACT ATT GAG GAA AAG GAG Lys Asp Gln Ile Lys Lys His Asp Ile Glu Thr Ile Glu Glu Lys Glu 475 480 485	1554
GAA GAT CTT AAG AGA GAA GAG GAA ATT GCC AAG CTA AAT AAC TCC AGT Glu Asp Leu Lys Arg Glu Glu Glu Ile Ala Lys Leu Asn Asn Ser Ser 490 495 500	1602
CCA AAT TCC AGT GGA GGA GTT AAA GAG GAT TGC ACT GCC TCC ATG GAA Pro Asn Ser Ser Gly Gly Val Lys Glu Asp Cys Thr Ala Ser Met Glu 505 510 515	1650
CCT TCA GCA ATT GAA CTC CCA GAT TAT TTG ATA AAA TAT ATC GCT ATC Pro Ser Ala Ile Glu Leu Pro Asp Tyr Leu Ile Lys Tyr Ile Ala Ile 520 525 530 535	1698
GTC TCC TAT GAG CAA CGC CAG AAT TAT AAG GAT GAC TTC AAT GCA GAG Val Ser Tyr Glu Gln Arg Gln Asn Tyr Lys Asp Asp Phe Asn Ala Glu 540 545 550	1746
TAT GAT GAG TAC AGA GCT TTG CAT GCC AGG ATG GAG ACT GTA GCT AGA Tyr Asp Glu Tyr Arg Ala Leu His Ala Arg Met Glu Thr Val Ala Arg 555 560 565	1794
AGA TTT ATC AAA CTA GAT GCA CAA AGA AAG CGC CTT TCT CCA GGC TCA Arg Phe Ile Lys Leu Asp Ala Gln Arg Lys Arg Leu Ser Pro Gly Ser 570 575 580	1842
AAA GAG TAT CAG AAT GTT CAT GAA GAA GTC TTA CAA GAA TAT CAG AAG Lys Glu Tyr Gln Asn Val His Glu Glu Val Leu Gln Glu Tyr Gln Lys 585 590 595	1890
ATA AAG CAG TCT AGT CCC AAT TAC CAT GAA GAA AAA TAC AGA TGT GAA Ile Lys Gln Ser Ser Pro Asn Tyr His Glu Glu Lys Tyr Arg Cys Glu 600 605 610 615	1938
TAT CTT CAT AAC AAG CTG GCT CAC ATC AAA AGG CTA ATA GGT GAA TTT Tyr Leu His Asn Lys Leu Ala His Ile Lys Arg Leu Ile Gly Glu Phe 620 625 630	1986
GAC CAA CAG CAA GCA GAG TCA TGG TCC TAGAACTCTG CTTGGACCAG Asp Gln Gln Gln Ala Glu Ser Trp Ser 635 640	2033
AAGATGTGAA TAAACTTAAG CTTATTATT TAAAATTCCA AATGAGTTGC TCTAGATTCT AAAAAGGTGA AACTTGGCT GTTGAAAGTT TCAGTATTAG TAAACT	2093
	2139

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 640 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Gly Gly Thr Gly Gly Leu Arg Glu Glu Gln Arg Tyr Gly  
1 5 10 15

Leu Ser Cys Gly Arg Leu Gly Gln Asp Asn Ile Thr Val Leu His Val  
20 25 30

Lys Leu Thr Glu Thr Ala Ile Arg Ala Leu Glu Thr Tyr Gln Ser His  
35 40 45

Lys Asn Leu Ile Pro Phe Arg Pro Ser Ile Gln Phe Gln Gly Leu His  
50 55 60

Gly Leu Val Lys Ile Pro Lys Asn Asp Pro Leu Asn Glu Val His Asn  
65 70 75 80

Phe Asn Phe Tyr Leu Ser Asn Val Gly Lys Asp Asn Pro Gln Gly Ser  
85 90 95

Phe Asp Cys Ile Gln Gln Thr Phe Ser Ser Ser Gly Ala Ser Gln Leu  
100 105 110

Asn Cys Leu Gly Phe Ile Gln Asp Lys Ile Thr Val Cys Ala Thr Asn  
115 120 125

Asp Ser Tyr Gln Met Thr Arg Glu Arg Met Thr Gln Ala Glu Glu Glu  
130 135 140

Ser Arg Asn Arg Ser Thr Lys Val Ile Lys Pro Gly Gly Pro Tyr Val  
145 150 155 160

Gly Lys Arg Val Gln Ile Arg Lys Ala Pro Gln Ala Val Ser Asp Thr  
165 170 175

Val Pro Glu Arg Lys Arg Ser Thr Pro Met Asn Pro Ala Asn Thr Ile  
180 185 190

Arg Lys Thr His Ser Ser Ser Thr Ile Ser Gln Arg Pro Tyr Arg Asp  
195 200 205

Arg Val Ile His Leu Leu Ala Leu Lys Ala Tyr Lys Lys Pro Glu Leu  
210 215 220

Leu Ala Arg Leu Gln Lys Asp Gly Val Asn Gln Lys Asp Lys Asn Ser  
225 230 235 240

Leu Gly Ala Ile Leu Gln Gln Val Ala Asn Leu Asn Ser Lys Asp Leu  
245 250 255

Ser Tyr Thr Leu Lys Asp Tyr Val Phe Lys Glu Leu Gln Arg Asp Trp  
260 265 270

Pro Gly Tyr Ser Glu Ile Asp Arg Arg Ser Leu Glu Ser Val Leu Ser  
275 280 285

Arg Lys Leu Asn Pro Ser Gln Asn Ala Thr Gly Thr Ser Arg Ser Glu  
290 295 300

Ser Pro Val Cys Ser Ser Arg Asp Ala Val Ser Ser Pro Gln Lys Arg  
305 310 315 320

Leu Leu Asp Ser Glu Phe Ile Asp Pro Leu Met Asn Lys Lys Ala Arg  
325 330 335

Ile Ser His Leu Thr Asn Arg Val Pro Pro Thr Leu Asn Gly His Leu  
340 345 350

Asn Pro Thr Ser Glu Lys Ser Ala Ala Gly Leu Pro Leu Pro Pro Ala  
355 360 365

Ala Ala Ala Ile Pro Thr Pro Pro Pro Leu Pro Ser Thr Tyr Leu Pro  
370 375 380

Ile Ser His Pro Pro Gln Ile Val Asn Ser Asn Ser Asn Ser Pro Ser  
385 390 395 400

Thr Pro Glu Gly Arg Gly Thr Gln Asp Leu Pro Val Asp Ser Phe Ser  
405 410 415

Gln Asn Asp Ser Ile Tyr Glu Asp Gln Gln Asp Lys Tyr Thr Ser Arg  
420 425 430

Thr Ser Leu Glu Thr Leu Pro Pro Gly Ser Val Leu Leu Lys Cys Pro  
435 440 445

Lys Pro Met Glu Glu Asn His Ser Met Ser His Lys Lys Ser Lys Lys  
450 455 460

Lys Ser Lys Lys His Lys Glu Lys Asp Gln Ile Lys Lys His Asp Ile  
465 470 475 480

Glu Thr Ile Glu Glu Lys Glu Glu Asp Leu Lys Arg Glu Glu Glu Ile  
485 490 495

Ala Lys Leu Asn Asn Ser Ser Pro Asn Ser Ser Gly Gly Val Lys Glu  
500 505 510

Asp Cys Thr Ala Ser Met Glu Pro Ser Ala Ile Glu Leu Pro Asp Tyr  
515 520 525

Leu Ile Lys Tyr Ile Ala Ile Val Ser Tyr Glu Gln Arg Gln Asn Tyr  
530 535 540

Lys Asp Asp Phe Asn Ala Glu Tyr Asp Glu Tyr Arg Ala Leu His Ala  
545 550 555 560

Arg Met Glu Thr Val Ala Arg Arg Phe Ile Lys Leu Asp Ala Gln Arg  
565 570 575

Lys Arg Leu Ser Pro Gly Ser Lys Glu Tyr Gln Asn Val His Glu Glu  
580 585 590

Val Leu Gln Glu Tyr Gln Lys Ile Lys Gln Ser Ser Pro Asn Tyr His  
595 600 605

Glu Glu Lys Tyr Arg Cys Glu Tyr Leu His Asn Lys Leu Ala His Ile  
610 615 620

Lys Arg Leu Ile Gly Glu Phe Asp Gln Gln Ala Glu Ser Trp Ser  
625 630 635 640

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAATTAACCC TCATAAAGGG AAC

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAAGTTCA CCTTTAGAA TCTAGAGCAA CTC

33

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGGTGTCGA CGAGGAGCAG CGCTATGGGC TGCGTGCAG AC

42

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGTGGATCC TCATCACTAG GACCATGACT CTGCTTGCTG TTG

43

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 621 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ala Leu Lys Glu Asp Arg Ser Tyr Gly Leu Ser Gly Gly Arg  
1 5 10 15

Val Ser Asp Gly Ser Lys Val Ser Val Phe His Val Lys Leu Thr Asp  
20 25 30

Ser Ala Ile Arg Ala Phe Glu Ser Tyr Arg Ala Arg Gln Asp Ser Val  
35 40 45

Ser Leu Arg Pro Ser Ile Arg Phe Gln Gly Ser Gln Gly His Ile Ser  
50 55 60

Ile Pro Gln Pro Asp Cys Pro Ala Glu Ala Arg Thr Phe Ser Phe Tyr  
65 70 75 80

Leu Ser Asn Ile Gly Arg Asp Asn Pro Gln Gly Ser Phe Asp Cys Ile  
85 90 95

Gln Gln Tyr Val Ser Ser His Gly Glu Val His Leu Asp Cys Leu Gly  
100 105 110

Ser Ile Gln Asp Lys Ile Thr Val Cys Ala Thr Asp Asp Ser Tyr Gln  
115 120 125

Lys Ala Arg Gln Ser Met Ala Gln Ala Glu Glu Ile Arg Ser Arg  
130 135 140

Ser Ala Ile Val Ile Lys Ala Gly Gly Arg Tyr Leu Gly Lys Lys Val  
145 150 155 160

Gln Phe Arg Lys Pro Ala Pro Gly Ala Thr Asp Ala Val Pro Ser Arg  
165 170 175

Lys Arg Ala Thr Pro Ile Asn Leu Ala Ser Ala Ile Arg Lys Ser Gly  
180 185 190

Ala Ser Ala Val Ser Gly Gly Ser Gly Val Ser Gln Arg Pro Tyr Arg  
195 200 205

Asp Arg Val Ile His Leu Leu Ala Leu Arg Pro Tyr Arg Lys Ala Glu  
210 215 220

Leu Leu Leu Arg Leu Gln Lys Asp Gly Leu Thr Gln Ala Asp Lys Asp  
225 230 235 240

Ala Leu Asp Gly Ile Leu Gln Gln Val Ala Asn Met Ser Ala Lys Asp  
245 250 255

Gly Thr Cys Thr Leu Gln Asp Cys Met Tyr Lys Asp Val Gln Lys Asp

260	265	270
Trp Pro Gly Tyr Ser Glu Gly Asp Gln Gln Leu Leu Lys Arg Val Leu		
275	280	285
Val Arg Lys Leu Cys Gln Pro Gln Ser Thr Gly Ser Leu Leu Gly Asp		
290	295	300
Pro Ala Ala Ser Ser Pro Pro Gly Glu Arg Gly Arg Ser Ala Ser Pro		
305	310	315
320		
Pro Gln Lys Arg Leu Gln Pro Pro Leu Phe Ile Asp Pro Leu Ala Asn		
325	330	335
Lys Lys Pro Arg Ile Ser His Phe Thr Gln Arg Ala Gln Pro Ala Val		
340	345	350
Asn Gly Lys Leu Gly Val Pro Asn Gly Arg Glu Ala Leu Leu Pro Thr		
355	360	365
Pro Gly Pro Pro Ala Ser Thr Asp Thr Leu Ser Ser Ser Thr His Leu		
370	375	380
Pro Pro Arg Leu Glu Pro Pro Arg Ala His Asp Pro Leu Ala Asp Val		
385	390	395
400		
Ser Asn Asp Leu Gly His Ser Gly Arg Asp Cys Glu His Gly Glu Ala		
405	410	415
Ala Ala Pro Ala Pro Thr Val Arg Leu Gly Leu Pro Leu Leu Thr Asp		
420	425	430
Cys Ala Gln Pro Ser Arg Pro His Gly Ser Pro Ser Arg Ser Lys Pro		
435	440	445
Lys Lys Lys Ser Lys Lys His Lys Asp Lys Glu Arg Ala Ala Glu Asp		
450	455	460
Lys Pro Arg Ala Gln Leu Pro Asp Cys Ala Pro Ala Thr His Ala Thr		
465	470	480
Pro Gly Ala Pro Ala Asp Thr Pro Gly Leu Asn Gly Thr Cys Ser Val		
485	490	495
Ser Ser Val Pro Thr Ser Thr Ser Glu Thr Pro Asp Tyr Leu Leu Lys		
500	505	510
Tyr Ala Ala Ile Ser Ser Ser Glu Gln Arg Gln Ser Tyr Lys Asn Asp		
515	520	525
Phe Asn Ala Glu Tyr Ser Glu Tyr Arg Asp Leu His Ala Arg Ile Glu		
530	535	540
Arg Ile Thr Arg Arg Phe Thr Gln Leu Asp Ala Gln Leu Arg Gln Leu		
545	550	560
Ser Gln Gly Ser Glu Glu Tyr Glu Thr Thr Arg Gly Gln Ile Leu Gln		
565	570	575
Glu Tyr Arg Lys Ile Lys Lys Thr Asn Thr Asn Tyr Ser Gln Glu Lys		
580	585	590

His Arg Cys Glu Tyr Leu His Ser Lys Leu Ala His Ile Lys Arg Leu  
595 600 605

Ile Ala Glu Tyr Asp Gln Arg Gln Leu Gln Ala Trp Pro  
610 615 620

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Trp Ile Arg Glu Tyr Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln  
1 5 10 15

Leu Tyr Lys Arg Asn Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu  
20 25 30

Gln Ser Glu Leu Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys  
35 40 45

Glu Leu Asp Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala  
50 55 60

Asp Glu Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys  
65 70 75 80

Ser Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile  
85 90 95

Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCCACCGCT GCCTTCAACC TATCTGCCA TCTCACATCC TCCTCAGATT GTAAATTCTA 60

ACTCCAACTC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT 120

TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATAACCTCT AGGACTTCTC	180
TGGAAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTCC AAAGCCTATG GAAGAAAACC	240
ATTCAATGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC	297

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA	60
ATTCGGAAAG CACCTCAAGC TGTTTCAGAT ACAGTTCCCTG AGAGGAAAAG GTCAACCCCC	120
ATGAACCCCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA	180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAACC GGAGCTACTT	240
GCTAGACTCC AGAAAAGATGG TGTCAATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN	300
TTGCAACAGG TAGNCCAATC TGGATTCTA AGGGACCTCT TCATATTACC TTTAAAGG	358

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCGNCGTNN TCGNCGGGCA CCCCAGGGAG TTTGAAGATG GCGGCGGGGG GGACAGGGGG	60
CCTNCGGGAG GAGCAGCGCT ATGGGCTGTC GTGCCGGACG GCTGGGGCAG GACAACATCA	120
CCGTACTGCA TGTNAAGCT TCACCGAGAC GGNCGATTCC GGGCGGGTTC GAGAACTTAC	180
CAGAGCCACA AGNNTTNAA TTCCCTTTTC GGACCTTCAA TCCAGTTCC AAGGACTCCA	240
CGGGCTTGT NCAAAATTT CCCAAAAATG ATTCCCCTTC AATGGANAGT TCATAAAATTT	300
TAAATTTTA ATTTGTTCAA ATNTTGGGN AAAGNCAAAC CTTCAAGGGC NAGTTTGGA	360
CT	362

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTCGGCAC GAGCATGGTC CTAGAACTCT GCTTNGACCA GAAGATGTGA ATAAACTTAA	60
GCTTATTAT TTAAAATTCC AAATGAGTTN NTCTAGNTTC TAAAAAGGTG AAACCTTGCG	120
TGTTGAAAGT TTCAGTATTA GTAAAATTGA GTTACTTTNN CTTTCCATT TNACTTTGCT	180
TCCCTGCATT TCGAAGCTGC TCTTCTGGT CCTCCCCACC ACCCCACCCC CAAGACTTGT	240
GTTTGTAAAT AGAAAATAATT TTTTAGGTA TTGGGGATCC ATTGTCTATT ATTCAAATC	300
AAGNTTTTN TTTNTCCTCA AAAANCTGT GGTTTGTGA TTAGGAAATG GNTTTTTAG	360
ATATTGGGGN TCCAGTGTCC NCAC TGAAA AGGTGGGNAG GGGTTTAAAA AANAGCANCA	420
GTAATNTGCA AGGTGNAATG NTTTGGTNA ACGGANGCCA TTTTCCGACG TNCTTAA	477

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAACATTCTC CAGCTCTGGG ACCTCCANC TCAATTCCCT GGGATTNAT ACAAGATAAA	60
ATTACAGTGT GTGCACAAAC GACTCGTATC AAATGACACG AGAAANANTG ACCCAGGCAG	120
NGGAGGGAAAT CCCGCAACCA ANGCACAAAAA GTTATTCAAACCCGGTGGGA CCATATNT	178

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GNCCCTTCTC CANTCTCAAA AGNGNTATCA CAATGTTCAT GNAAGAAGTC TTACAAGAAT	60
ATCAGAAAGAT AAAGCCAGTC TAGTCCAAT TACCATGAAG NAAAAATACA GATGTGNAAT	120
ATCTTCATAA CAAGCTGGCT CACATCAAAA GGCTAATN	158

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATAAATAAGC TTAAGTTAT TCACATCTTC TGGTCCAAGC AGAGTTCTAG GACCATGACT	60
CTGCTTGCTG TTGGTCAAAT TCACCTATT A GCCTTTGAT GTGAGCCAGC TTGTTATGAA	120
GATATTACACA TCTGTATT TCTTCATGGT AATTGGGACT AGACTGCTT ATCTTCTGAT	180
ATTCTTGTAAGACTTCTCA TGAACATTCT GATACTCTT TGAGCCTGGA GAAAGGCGCT	240
TTCTTTGTGC ATCTAGTTG ATAAATCTTC TAGCTACAGT CTCCATCCTG GCATGCAAAG	300
CTCTGTACTC ATCATACTCT GCATTGAAGT CATCCTTATA ATTCTGGCGT TGCTCATAGG	360
AGACGATAGC GATATATTTT ATCAAATAAT CTGGGAGTTC AATTGCTGAA GGGTCCATGG	420
AGGCAGTGCA ATCCTCTT	438

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGNCCGCAG TGGANGGCTA GAGCGNAGCG CGCGGCGGGCG GNCACCCCGG GGAGTTAAC	60
ATGGCGGCNG GGGGGACAGG GGGCCTGCAG GAGGAGCAGC GCTATGGGCT GTCGTGCGGA	120
CGGCTGGGGC AGGACAACAT CACCGTACTG CATGTGAAGC TCACCGAGAC GGCAGATCCGG	180

GCGCTCGAGA CTTACCAGAG CCACAAGAAT TTAATTCCCTT TTGACCTTC AATCCAGTTC	240
CAAGGACTCC ACGGGCTTGT CAAAATTCCC AAAATGATC CCCTCAATGA AGTCATAAC	300
TTTAACCTTT ATTTGTCAAA TGTGGGCAAA GACAACCCTC AGGGCAAGCT TTGACTGCAT	360
CCAGCAAACA TTCTCCAGCT CTGGAGCCTC CCAGCTCAAT TGCCTNGGGA TTTATACAAG	420
ATAAAATTAC AGTGTGTGCA ACAAACGACT CGTATCAGA	459

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGATTCAA ATGACCATTG AGTGTGGTG GTACTCTGTT CGTCAGGTGA GATATTCGGG	60
CTTTTTATT CATAAAGGA TCAATAAACT CTGAATCCAA AAGCCGTTTC TGAGGAGAAAG	120
ATACAGCATC TCTACTAGAA CATAcAGGAG ATTCTGAACG GCTGGTGCCT GTAGCATTCT	180
GAGACGGATT TAGTTTCTA GAGAGCACTG ACTCCAATGA CCGTCTGTCT ATTCACTGT	240
ATCCAGGCCA GTCTCTTGA AGCTCTTAA AACATAATC CTTAAGGGA TATGAGAGGT	300
CCTTAGAATT CAGATTGGCT AGCTGTTGCA GAATTGCTCC CAGGGAGTTC TTGCTTTTT	360
GATTGACACC ATCTTCTGG AGTCCTACAA GTAGCTCCGG GTTTCTTGTAA GG	412

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAATAAAAG AAACCTGACA TTGAGACCAC GGAGGGAGAAG GAGGAAGACC TTCAGAGAGA	60
AGAAACTGCC AAGCTGAGTA ATGCCAGTCC AAATCCAAT GAAGGAGTTA AAGAAGGGTG	120
CACAGCCTCC ATGGAGCCTT CTTCAAGCACT TGAACCCCCA GATTATTGAA TAAAATATAT	180
TGCTATTGTC TCTTATGAGC AACGCCAGAA TTACAAGGAT GACTTCAATG CTGAGTATGA	240

TGAATACAGA GCTTGATG CAAGGATGGA GACTGTAGCC AGGAGATTAA TTAAACTGGA	300
TGCACAAACGA AAACGCCCTT CTCCAGGTTC AAAAGAGTAC CAGAATGTTC ATGAAGAAGT	360
CTTACAGGAA TATCAGAAGA TCAAGCAGTC CAGTCCAAT TACCATGAAG AAAAATACAG	420
ATGTGAATAT CTTCTATAACA AGCTGGCTCA CATCAAAGAC TAATAGGTG AATTTGACCA	480
ACAGCAA	487

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCTTGATG CCAGGATGGA GACTGTAGCT AGAAGATTAA TCAAACCTAGA TGCACAAAGA	60
AAGGCCCTT CTCCAGGCTC AAAAGAGTAT CAGAATGTTC ATGAAGAAGT CTTACAAGAA	120
TATCAGAAGA TAAAGCAGTC TAGTCCAAT TACCATGAAG AAAAATACAG ATGTGAATAT	180
CTTCTATAACA AGCTGGCTCA CATCAAAGG CTAATAGGTG AATTTGACCA ACAGCAAGCA	240
GAGTCATGGT CCTAGAACTC TGCTTGGACC AGAAGATGTG AATAAACTTA AGCTTATTAA	300
TTTAAAATTC CAAATGAGTT GCTCTAGATT CTAAAAAGGT GAAACTTGG CTGTTGAAAG	360
TTTCAGTATT AGTAAACTTN GAGTTACTTT TTCTTTCCA TTTTACTTTG CTTCCCTGCA	420
TTTCGGAAGC TGCCTCTTTN CTGGGTCCCTC NCCACTNGGG GCCAGCCCC AAGNACTTGG	480
TGTTTGGTT AATAGGNAAT AATTTCTTT AAGGGAAATTG GGGGA	525

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTAGTCAAAA TGGTAGCATC TTTGAGGACC AGCAAGAAAA ATATACCTCA AGGACTTGTC	60
TGGAAACATT ACCCCCCAGC TCAGCTCTGC TAAAGTGTCC AAAGCCCATG GAAGAAGAGC	120

ATCCAGTGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACACAAGGAA AAGGACCAAA	180
TAAAGAAACT TGACATTGAG ACCATGGAGG AGAAGGAGGA AGACCTTCAG AGAGAAGAAA	240
CTGCCAAGCT GAGTAATGCC AGTCAAATC CCAATGAAGG AGTTAAAGAA GGGTGCACAG	300
CCTCCATGGA GCCTTCTTCA GCACTTAAC CAGAATTACA AGGATGACTT CAATGCTGAG TATGATGAAT	360
TTGTCTCTTA TGAGCAACGC CAGAATTACA AGGATGACTT CAATGCTGAG TATGATGAAT	420
ACAGAGCTTT GCATGCAAGG ATGGAGACTG TAGCG	455

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCACTTACTG GCCCTGAAGG CTACAAGAAA CGGGAGCTAC TTGCTAGACT CCAGAAAGAT	60
GGTGTCAATC AAAAGACAA GAACTCCCTG GGAGCAATT TGCAACAGGT AGCCAATCTG	120
AATTCTAAGG ACCTCTCAT AACTTAAAG GATTATGTTT TTAAAGAGCT TCAAAGAGAC	180
TGGCCTGGNT ACAGTGAAAT AGACAGACGG TCATTGGAGT CAGTGCTCTC TAGAAAAC	240
AATCCGTCTC AGAATGCTAC AGGCACCAGC CTNTCAGAAT CTCCTGTATG TTCTAGTAGA	300
GATGCTGTAT CTTCTCCTCA GGAAACGGCT TTTGGTTTC AGAGTTTATT TGATCCCTT	360
AATGGANTTA AAAAGGCT	379

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 519 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NTCACTTACT GGCCCTGAAG CTANCAAGAA ACCGGAGCTA CTTGCTAGAC TCCAGAAAGA	60
TGGTGTCAAT CAAAAAGACA AGAACTCCCT GGGAGCAATT CTGCAACAGG TAGCCAATCT	120
GAATTCTAAG GACCTCTCAT ATACCTTAAA GGATTATGTT TTTAAAGAGC TTCAAAGAGA	180

CTGGCCTGGG ATACAGTGAA ATAGACAGAC GGTCAATTGGA GTCAGTGCTC TCTAGAAAAC	240
TAAATCCGTC TCAGAATGCT ACAGGCACCA GCGTTTCAGA ATCTCCTGTA TGTTCTAGTA	300
GGAGATGCTG TATCTTCTCC TCAGGAAACG GCTTTGGGT TCAGGAGTTT ATTTGATCCN	360
TTTAATGGAT TAAAAAAAGGC CCCGATTATT CTTCACCTGG ACGGAACAGA GTTACCNCCC	420
AACATTAATG GGTCCNTTG GATTCCCACC AGTGGAAAAT TGGGTGGCGG GCTTNCCCAT	480
TGCCCTGNG GGTGGTGGCN TTCCCCACCC TTNCACCGG	519

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 297 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCCACCGCT GCCTTCAACC TATCTGCCCA TCTCACATCC TCCTCAGATT GTAAATTCTA	60
ACTCCAACTC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT	120
TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATAACCTCT AGGACTTCTC	180
TGGAAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTCC AAAGCCTATG GAAGAAAACC	240
ATTCAATGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC	297

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 358 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA	60
ATTCGGAAAG CACCTCAAGC TGTTTCAGAT ACAGTTCTG AGAGGAAAAG GTCAACCCCC	120
ATGAACCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA	180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAAACC GGAGCTACTT	240
GCTAGACTCC AGAAAGATGG TGTCAATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN	300

TTGCAACAGG TAGNCCAATC TGGATTCTA AGGGACCTCT TCATATTACC TTTAAAGG 358

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 285 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTGAGA CATTGAATGG TTTTCTCCA TAGGCTTGG ACACTTAGT AGAACGGAAC 60  
CAGGGGTAA GGTTCCAGA GAAGTCCTAG AGGTATATT GTCTTGCTGG TCCTCATAGA 120  
TACTATCGTT TTGACTAAAA CTNTCAACAG GTAGGTCTTGTAGT CTTCTGGAG 180  
TGCTAGGGGA GTTGGAGTTA GAATTACAA TCTGAGGAGG ATGTGAGATG GGCAGATAGG 240  
TTGAAGGCAG CGGTGGAGGG GTGGGGATGG CAGCAGCCCA GGGGG 285

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 431 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTTATTCCAA ACAGCATCAT CTACAACCTCA TAATCGCAGG CTCCTCCAGT TCATTAAACA 60  
CAGAAAGCAG GCTTTTTCT CTTTCCCCTTAAACAAAT GTAAAATACC TTCATTGGGA 120  
TTTGGACTGG CATTACTCAG CTTGGCAGTT TCTTCTCTCT GAAGGTCTTC CTCCTCTCC 180  
TCCATGGTCT CAATGTCAAG TTTCTTATT TGGTCCTTTT CCTTGTGTTT TTTAGACTTC 240  
TTTTGGACT TTTGTGAGA CACTGGATGC TCTTCTTCCA TGGGCTTGG ACACTTAGC 300  
AGAGTGAGCT GGGGGTAAT GTTTCCAGAC AAGTCCTTGA GGTATATTTT TCTTGCTGGT 360  
CCTCAAAGAT GCTACCATT TGACTAAAAC TGTCAACAGG CAGGTCTTGA GTCCCAGGCC 420  
TTCTGGAGTG C 431

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CACCGAGACG GCGATCCGGG CGCTCGAGAC TTACCAGAGC CACAAGAATT TAATTCCTTT	60
TCGACCTTCA ATCCAGTTCC AAGGACTCCA CGGGCTTGTC AAAATTCCCA AAAATGATCC	120
CCTCAATGAA GTTCATAACT TTAACTTTA TTTGTCAAAT GTGGGCAAAG ACAACCCCTCA	180
GGGGAGCTTG GGCTGC	196

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 197 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCATCTCTC AGAGGCCATA CAGGGACAGG GTGATTCACT TACTGGCCCT GAAGGCNTAC	60
AAGAAACCGG AGCTACTTGC TAGACTCCAG AAAGATGGTG TCAATCAAAA AGACAAGAAC	120
TCCCTGGGAG CAATTCTGCA ACAGGTAGCC AATCTGAATN CTAAGGACCT CNTCATATAAC	180
CTTAAAGGAT TATGTTT	197

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCGCCCGGCA GTGGAGGCTA GAGCCGCAGC GCGCGGCGGG CGGACACCGC CGGGGAGGTT	60
TAAGAGTGGC GGCTGGGGGG GACAGGGGG CCTGCAGGGA GGAGCAGCGC TATGGGCTGT	120
CGTGCAGGACG GCGTGGGGCA GGACAACATC ACCGTACTGC ATGTGAAGCT CACCGAGACG	180

GCGATCCGGG CGCTCGAGAC TTACCAGAGC CACAAGAATT TAATTCCATT TCGACCTTCA	240
ATCCAGTTCC AAGGACTCCA CGGGGTGAGT ACTCTTATTG ATTTAACAAA CAAATCTAAT	300
GTTCTTGCAC GCTATTCAAC TTTTAAAATC CGTTTCAGT TGACCCTT	348

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGGAATTTAA ATAAATAAGC TTAAGTTAT TCACATCTNC TGGTCCAAGC AGAGTTCTAG	60
GACCATGACT CTGCTTGCTG TTGGTCAAAT TCACCTATTAA GCCTTNGAT GTGAGCCAGC	120
TGTTATGAA GATATTACAA TCTGTATTT NCTTCATGGT AATTGGGACT AGACTGCTTT	180
ATCT	184

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT ATTTAAAATC	60
ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG ACTGTTGAAA GTTTAAGTAT	120
TAGTAAACTT GAGTTACTTT TTCTTTCAAA TTTCACTCCG CTTCCCTGCA TTTCGAAGCT	180
GCTCTTCTG GTCCTACCCA CCACCCCCACC AACAAAGACTT GTGTTGTTA ATAGAAATAA	240
TTTATCAAGG TATTGGGGAT CCATTGTCTA TATTAAAAC	280

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AACTAGCAGT CCCTTGCGGC CAATTGATGT AATTATTTTC AGTGTAAATC CNAAAGGTTG	60
CCTGTTTAN GNTAGGAGAT GATA GTAAAAA ATACCTAATG CTCTGTTTT ATACCTCATA	120
CTAGGTAGCC AATCTGAATT CTAAGGACCT CTCATATACC TTAAAGGATT ATGTTNTAA	180
AGAGCTTCAA AGAGACTGGC CTGGATACAG TGAAATAGAC AGACGGTCAT TGGAGTCATG	240
TGCTCTCTAG GTGAA	255

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACCTAAC TGAGTAGGGC GTCCGATCGA CGGACGCCCTT TTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTCCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAA GCCTGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA	240
TCGGCCAACG CGCGGGGAGA GGCGGTTGC GTATTGGCG CTCTTCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC	420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAC CCGACAGGAC	540
TATAAAAGATA CCAGGCCTTT CCCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACCGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCAGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900

GAAGAACAGT ATTTGGTATC TCGCCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTT GTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTT TCTACGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA	1140
CAATTCCGCGC CGCAAGGCCGA AGCGGCATGC ATTACGTTG ACACCATCGA ATGGTGCAA	1200
ACCTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAAGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT TCCCACCGC GTGGCACAAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTCGCG	1500
CGCATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAAGCAGGCCGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTAACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTCT TGATGTCCT GACCAGACAC CCATCAACAG TATTATTTCT	1740
TCCCATGAAG ACGGTACGCG ACTGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGCGC GTCTGCGTCT GGCTGGCTGG	1860
CATAAAATATC TCACTCGCAA TCAAATTCAAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCACTGCG	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GGCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACAC CATCAAACAG GATTTCGCC TGCTGGGCA AACCAAGCGTG	2160
GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTGCCCCGTC	2220
TCACTGGTGA AAAGAAAAAC CACCCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAAGTACGAA ATTGTCGACC AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTTGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC	2460
GACGGATTTG CACTGCCGGT AGAAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCCCCGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG	2580
CTGGAGGATC ATCCAGGCCGG CGTCCCGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGC GTCGCTTGGT CGGTCAATTTC	2700
GAACCCCAGA GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760

GAATCGGGAG CGGCGATAACC GTAAAGCACG AGGAAGCGGT CAGCCCATTG GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTCCA CCATGATATT CGGCAAGCAG	2940
GCATGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCAGCCCTT GAGCCTGGCG	3000
AACAGTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCGA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTAGC TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCAG TGCCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTGCAG TGCGTGTTC CCTTGTCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCAGTT TCTGCGGACT GGCTTCTAC GTGTTCCGCT TCCTTAGCA GCCCTGCGC	3840
CCTGAGTGCT TGCAGGAGCG TGAAGCTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTCACAC ATAAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGCTTAAAA AACTGCAAAA AATAGTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGGAG AAATTACATA TG	112